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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/965,825

DATE: 11/07/2001

TIME: 14:41:53

Input Set : A:\es.txt

Output Set: N:\CRF3\11072001\I965825.raw

2

3 <110> APPLICANT: DUSCH, Nicole
 4 THOMAS, Hermann
 5 THIERBACH, Georg
 7 <120> TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF D-PANTOTHENOIC
 ACID USING
 8 CORYNEFORM BACTERIA
 10 <130> FILE REFERENCE: 21354US0X
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/965,825 *ov*
 C--> 12 <141> CURRENT FILING DATE: 2001-10-01
 12 <150> PRIOR APPLICATION NUMBER: DE 10048604.5
 13 <151> PRIOR FILING DATE: 2000-09-30
 15 <150> PRIOR APPLICATION NUMBER: DE 10117085.8
 16 <151> PRIOR FILING DATE: 2001-04-06
 18 <160> NUMBER OF SEQ ID NOS: 14
 20 <170> SOFTWARE: PatentIn version 3.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2160
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Corynebacterium glutamicum
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 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (327)..(2063)
 30 <223> OTHER INFORMATION:
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 35 <222> LOCATION: (227)..(232)
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 48 cgaggcgacc agacaggcgt gccacgatg tttaaataagg cgatcgggtg gcatctgtgt 120
 50 ttgggtttcga cgggctgaaa ccaaaccaga ctgccagca acgacggaaa tcccaaaagt 180
 52 gggcatccct gtttgtacc gaggaccac cgggacctga aactccctgg caggcgggag 240
 54 aagcgtggca acaactggaa tttaagagca caattgaagt cgcaccaagt taggcaacac 300
 56 aatagccata acgttgagga gttcag atg gca cac agc tac gca gaa caa tta 353
 57 Met Ala His Ser Tyr Ala Glu Gln Leu
 58 1 5
 60 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 401
 61 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 62 10 15 20 25
 64 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 449
 65 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 66 30 35 40
 68 gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg ttt gca gcc ggt 497
 69 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly

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70	45	50	55	
72	gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt	545		
73	Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys			
74	60 65 70			
76	ggt cct gga aac aca cac ctg att cag ggt ctt tat gat tcg cat cga	593		
77	Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg			
78	75 80 85			
80	aat ggt gcg aag gtg ttg gcc atc gct agc cat att ccg agt gcc cag	641		
81	Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln			
82	90 95 100 105			
84	att ggt tcg acg ttc ttc cag gaa acg cat ccg gag att ttg ttt aag	689		
85	Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu Ile Leu Phe Lys			
86	110 115 120			
88	gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt gag cag ggt gaa	737		
89	Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly Glu Gln Gly Glu			
90	125 130 135			
92	cgc att ttg cat cac gcg att cag tcc acc atg gcg ggt aaa ggt gtg	785		
93	Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala Gly Lys Gly Val			
94	140 145 150			
96	tcg gtg gta gtg att cct ggt gat atc gct aag gaa gac gca ggt gac	833		
97	Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu Asp Ala Gly Asp			
98	155 160 165			
100	ggt act tat tcc aat tcc act att tct tct ggc act cct gtg gtg ttc	881		
101	Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe			
102	170 175 180 185			
104	ccg gat cct act gag gct gca gcg ctg gtg gag gcg att aac aac gct	929		
105	Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala Ile Asn Asn Ala			
106	190 195 200			
108	aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag aat gct cgc gcg	977		
109	Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala			
110	205 210 215			
112	cag gtg ttg gag ttg gcg gag aag att aaa tca ccg atc ggg cat gcg	1025		
113	Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala			
114	220 225 230			
116	ctg ggt ggt aag cag tac atc cag cat gag aat ccg ttt gag gtc ggc	1073		
117	Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro Phe Glu Val Gly			
118	235 240 245			
120	atg tct ggc ctg ctt ggt tac gcc gcc tgc gtg gat gcg tcc aat gag	1121		
121	Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu			
122	250 255 260 265			
124	gcg gat ctg ctg att cta ttg ggt acg gat ttc cct tat tct gat ttc	1169		
125	Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe			
126	270 275 280			
128	ctt cct aaa gac aac gtt gcc cag gtg gat atc aac ggt gcg cac att	1217		
129	Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile			
130	285 290 295			
132	ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt gat gtt gct gca	1265		
133	Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala			
134	300 305 310			

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136	aca atc gaa aat att ttg cct cat gtg aag gaa aaa aca gat cgt tcc	1313
137	Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys Thr Asp Arg Ser	
138	315 320 325	
140	ttc ctt gat cgg atg ctc aag gca cac gag cgt aag ttg agc tcg gtg	1361
141	Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys Leu Ser Ser Val	
142	330 335 340 345	
144	gta gag acg tac aca cat aac gtc gag aag cat gtg cct att cac cct	1409
145	Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val Pro Ile His Pro	
146	350 355 360	
148	gaa tac gtt gcc tct att ttg aac gag ctg gcg gat aag gat gcg gtg	1457
149	Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val	
150	365 370 375	
152	ttt act gtg gat acc ggc atg tgc aat gtg tgg cat gcg agg tac atc	1505
153	Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile	
154	380 385 390	
156	gag aat ccg gag gga acg cgc gac ttt gtg ggt tca ttc cgc cac ggc	1553
157	Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser Phe Arg His Gly	
158	395 400 405	
160	acg atg gct aat gcg ttg cct cat gcg att ggt gcg caa agt gtt gat	1601
161	Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala Gln Ser Val Asp	
162	410 415 420 425	
164	cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt ggt ttg ggc atg	1649
165	Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly Gly Leu Gly Met	
166	430 435 440	
168	ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa ctt ccg ctg aag	1697
169	Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln Leu Pro Leu Lys	
170	445 450 455	
172	gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg aag ttg gag atg	1745
173	Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val Lys Leu Glu Met	
174	460 465 470	
176	ctc gtg gag gga cag cca gaa ttt ggt act gac cat gag gaa gtg aat	1793
177	Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn	
178	475 480 485	
180	ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg gta cgc atc acc	1841
181	Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr	
182	490 495 500 505	
184	gat ccg aag aaa gtt cgc gag cag cta gct gag gca ttg gca tat cct	1889
185	Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro	
186	510 515 520	
188	gga cct gta ctg atc gat atc gtc acg gat cct aat gcg ctg tcg atc	1937
189	Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile	
190	525 530 535	
192	cca cca acc atc acg tgg gaa cag gtc atg gga ttc agc aag gcg gcc	1985
193	Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe Ser Lys Ala Ala	
194	540 545 550	
196	acc cga acc gtc ttt ggt gga gga gta gga gcg atg atc gat ctg gcc	2033
197	Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala	
198	555 560 565	
200	cgt tcg aac ata agg aat att cct act cca tgatgattga tacacctgct	2083

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201 Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
202 570                               575
204 gttctcattg accgcgagcg cttaactgcc aacatttcca ggatggcagc tcacgccggt 2143
206 gcccatgaga ttgccct 2160
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210 <211> LENGTH: 579
211 <212> TYPE: PRT
212 <213> ORGANISM: Corynebacterium glutamicum
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217 1 5 10 15
220 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
221 20 25 30
224 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
225 35 40 45
228 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
229 50 55 60
232 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
233 65 70 75 80
236 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
237 85 90 95
240 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
241 100 105 110
244 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
245 115 120 125
248 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
249 130 135 140
252 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
253 145 150 155 160
256 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
257 165 170 175
260 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
261 180 185 190
264 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
265 195 200 205
268 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
269 210 215 220
272 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
273 225 230 235 240
276 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
277 245 250 255
280 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
281 260 265 270
284 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
285 275 280 285
288 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
289 290 295 300
292 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
293 305 310 315 320

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296 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
297          325          330          335
300 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
301          340          345          350
304 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
305          355          360          365
308 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
309          370          375          380
312 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
313 385          390          395          400
316 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
317          405          410          415
320 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
321          420          425          430
324 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
325          435          440          445
328 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
329          450          455          460
332 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
333 465          470          475          480
336 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
337          485          490          495
340 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
341          500          505          510
344 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
345          515          520          525
348 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
349          530          535          540
352 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
353 545          550          555          560
356 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
357          565          570          575
360 Pro Thr Pro
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365 <211> LENGTH: 875
366 <212> TYPE: DNA
367 <213> ORGANISM: Corynebacterium glutamicum
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374 gcaggtgacg gtacttattc caattccact atttcttctg gcaactcctgt ggtgttcccg 180
376 gatcctaactg aggctgcagc gctggtggag gcgattaaca acgctaagtc tgtcactttg 240
378 ttctgcggtg cgggcgtgaa gaatgctcgc gcgcagggtg tggagttggc ggagaagatt 300
380 aaatcaccga tcgggcacgc gctgggtggg aagcagtaca tccagcatga gaatccgttt 360
382 gaggtcggca tgtctggcct gcttggttac ggcgcctgcg tggatgcgtc caatgagggc 420
384 gatctgctga ttctattggg tacggatttc ccttattctg atttccttcc taaagacaac 480
386 gttgccccagg tggatatcaa cgggtgcgcac attgggtcgac gtaccacggg gaagtatccg 540
388 gtgaccgggtg atgttgctgc aacaatcgaa aatattttgc ctcatgtgaa ggaaaaaaca 600
390 gatcgttcct tccttgatcg gatgctcaag gcacacgagc gtaagttgag ctcggtggtg 660

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date